

CLAIMS

What is claimed is:

~~30. (New) A nucleic acid sequence for use in cloning and expressing a root specific nucleic acid sequence in a plant, selected from the group consisting of: a nucleic acid sequence of SEQ ID No. 1; a nucleic acid sequence complementary to SEQ ID No. 1; a nucleic acid sequence having a degree of identity of more than 70% to SEQ ID No. 1 or to the sequence complementary to SEQ ID No. 1; alleles of the nucleic acid sequence of SEQ ID No. 1; alleles of the complementary sequence; alleles of a nucleic acid sequence having a degree of identity of more than 70% to SEQ ID No. 1; and alleles of a nucleic acid sequence having a degree of identity of more than 70% to a sequence complementary to SEQ ID No. 1.~~

~~31. (New) A nucleic acid sequence for use in cloning and expressing a root specific nucleic acid sequence in a plant, selected from the group consisting of: a nucleic acid sequence of SEQ ID No. 2; a nucleic acid sequence complementary to SEQ ID No. 2; a nucleic acid sequence having a degree of identity of more than 70% to SEQ ID No. 2 or to the sequence complementary to SEQ ID No. 2; alleles of the nucleic acid sequence of SEQ ID No. 2; alleles of the complementary sequence; alleles of a nucleic acid sequence having a degree of identity of more than 70% to SEQ ID No. 2; and alleles of a nucleic acid sequence having a degree of identity of more than 70% to a sequence complementary to SEQ ID No. 2.~~

~~32. (New) A nucleic acid sequence for use in cloning and expressing a root specific nucleic acid sequence in a plant, selected from the group consisting of: SEQ ID Nos. 3-11; a nucleic acid sequence complementary to any of SEQ ID Nos. 3-11; a nucleic acid sequence having a degree of identity of more than 70% to any of SEQ ID Nos. 3-11; a nucleic acid sequence having a degree of identity of more than 70% to a sequence complementary to any of SEQ ID Nos. 3-11; alleles of the nucleic acid sequence of any of SEQ ID Nos. 3-11; alleles of a sequence complementary to any of SEQ ID Nos. 3-11; alleles of a nucleic acid sequence having a degree of~~

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identity of more than 70% to any of SEQ ID Nos. 3-11; and alleles of a nucleic acid sequence having a degree of identity of more than 70% to a sequence complementary to any of SEQ ID Nos. 3-11.

*A<sup>2</sup> cont'd*  
~~33.~~ (New) A nucleic acid sequence for use in cloning and expressing a root specific nucleic acid sequence in a plant, selected from the group consisting of: SEQ ID Nos. 12-15; a nucleic acid sequence complementary to any of SEQ ID Nos. 12-15; a nucleic acid sequence having a degree of identity of more than 70% to any of SEQ ID Nos. 12-15; a nucleic acid sequence having a degree of identity of more than 70% to a sequence complementary to any of SEQ ID Nos. 12-15; alleles of the nucleic acid sequence of any of SEQ ID Nos. 12-15; alleles of a sequence complementary to any of SEQ ID Nos. 12-15; alleles of a nucleic acid sequence having a degree of identity of more than 70% to any of SEQ ID Nos. 12-15; and alleles of a nucleic acid sequence having a degree of identity of more than 70% to a sequence complementary to any of SEQ ID Nos. 12-15.

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~~34.~~ (New) A nucleic acid sequence derived from maize for use in cloning and expressing a root specific nucleic acid sequence in a plant, the sequence being selected from the group consisting of: a nucleic acid sequence of any of SEQ ID Nos. 1-15; a nucleic acid sequence complementary to any of SEQ ID Nos. 1-15; a nucleic acid sequence having a degree of identity of more than 70% to any of SEQ ID Nos. 1-15 or to a sequence complementary to any of SEQ ID Nos. 1-15; alleles of the nucleic acid sequence of any of SEQ ID Nos. 1-15; alleles of a sequence complementary to any of SEQ ID Nos. 1-15; alleles of a nucleic acid sequence having a degree of identity of more than 70% to any of SEQ ID Nos. 1-15; and alleles of a nucleic acid sequence having a degree of identity of more than 70% to a sequence complementary to any of SEQ ID Nos. 1-15.

~~35.~~ (New) A vector comprising a nucleic acid sequence selected from the group consisting of:

a nucleic acid sequence of any of SEQ ID Nos. 1-15; a nucleic acid sequence complementary to any of SEQ ID Nos. 1-15; a nucleic acid sequence having a degree of identity of more than 70% to any of SEQ ID Nos. 1-15 or to a sequence complementary to any of SEQ ID Nos. 1-15; alleles of the nucleic acid sequence of any of SEQ ID Nos. 1-15; alleles of a sequence complementary to any of SEQ ID Nos. 1-15; alleles of a nucleic acid sequence having a degree of identity of more than 70% to any of SEQ ID Nos. 1-15; and alleles of a nucleic acid sequence having a degree of identity of more than 70% to a sequence complementary to any of SEQ ID Nos. 1-15.

36.(New) The vector of Claim 35, which is a bacterial or viral vector.

37.(New) The vector of Claim 35, wherein the nucleic acid sequence is operably linked to a gene of interest.

38. (New) The vector of Claim 37, wherein the gene of interest is a gene which confers a character of agronomic or industrial benefit.

39. (New) The vector of Claim 38, wherein the gene of interest is a gene for resistance to infection by a virus, a gene conferring resistance to an herbicide or insecticide, or a gene whose expression confers male sterility.

40.(New) The vector of Claim 37, which further includes regulatory elements directing or enhancing the expression of the gene of interest.

41.(New) The vector of Claim 40, wherein the regulatory elements are 5', 3', or 5' and 3' elements.

42. (New) The vector of Claim 41, wherein the 3' regulatory element is a poly A addition sequence of an NOS gene of *Agrobacterium tumefaciens*.

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503 > 43. (New) The vector of Claim 40, which further includes T-DNA.

44. (New) The vector of Claim 43, which includes the left border of T-DNA, the right border of T-DNA, or both the left and right borders of T-DNA.

45. (New) The vector of Claim 43, wherein the nucleic acid sequence is located within the T-DNA or adjacent to the T-DNA.

46. (New) The vector of Claim 45, wherein the nucleic acid sequence is in conjunction with the gene of interest and is located within the T-DNA or adjacent to it.

47. (New) A host cell containing a vector comprising a nucleic acid sequence selected from the group consisting of:  
a nucleic acid sequence of any of SEQ ID Nos. 1-15; a nucleic acid sequence complementary to any of SEQ ID Nos. 1-15; a nucleic acid sequence having a degree of identity of more than 70% to any of SEQ ID Nos. 1-15 or to a sequence complementary to any of SEQ ID Nos. 1-15; alleles of the nucleic acid sequence of any of SEQ ID Nos. 1-15; alleles of a sequence complementary to any of SEQ ID Nos. 1-15; alleles of a nucleic acid sequence having a degree of identity of more than 70% to any of SEQ ID Nos. 1-15; and alleles of a nucleic acid sequence having a degree of identity of more than 70% to a sequence complementary to any of SEQ ID Nos. 1-15.

48. (New) The host cell of Claim 47, wherein the nucleic acid sequence is operably linked to a gene of interest, and the gene of interest is a gene which confers a character of agronomic or industrial benefit.

49. (New) The host cell of Claim 48, wherein the gene of interest is a gene for resistance to infection by a virus, a gene conferring resistance to an herbicide or insecticide, or a gene whose expression confers male sterility.

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~~50.(New) The host cell of Claim 48, which further includes regulatory elements directing or enhancing the expression of the gene of interest.~~

51.(New) The host cell of Claim 50, wherein the regulatory elements are 5', 3', or 5' and 3' elements.

~~52.(New) The host cell of Claim 51, wherein the 3' regulatory element is a poly A addition sequence of an NOS gene of Agrobacterium tumefaciens.~~

53.(New) The host cell of Claim 50, which further includes T-DNA.

54.(New) The host cell of Claim 53, which includes the left border of T-DNA, the right border of T-DNA, or both the left and right borders of T-DNA.

55. (New) The host cell of Claim 54, wherein the nucleic acid sequence is located within the T-DNA or adjacent to the T-DNA.

~~56. (New) The host cell of Claim 53, wherein the nucleic acid sequence is in conjunction with the gene of interest and is located within the T-DNA or adjacent to it.~~

57.(New) The host cell of Claim 47, which is a plant, yeast, or bacterial cell.

58.(New) The host cell of Claim 57, which is a cell from a monocotyledonous or dicotyledonous plant.

~~59.(New) A cell culture including a host cell selected from the group consisting of plant, yeast and bacterial cells; said host cell containing a vector comprising a nucleic acid sequence selected from the group consisting of:  
a nucleic acid sequence of any of SEQ ID Nos. 1-15; a nucleic acid sequence complementary to any of SEQ ID Nos. 1-15; a nucleic acid sequence having a degree of identity of more than 70% to any of SEQ ID Nos. 1-15 or to a sequence~~

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complementary to any of SEQ ID Nos. 1-15; alleles of the nucleic acid sequence of any of SEQ ID Nos. 1-15; alleles of a sequence complementary to any of SEQ ID Nos. 1-15; alleles of a nucleic acid sequence having a degree of identity of more than 70% to any of SEQ ID Nos. 1-15; and alleles of a nucleic acid sequence having a degree of identity of more than 70% to a sequence complementary to any of SEQ ID Nos. 1-15.

*A<sup>1</sup> cont'd*  
~~60.~~(New) A plant including a host cell containing a vector comprising a nucleic acid sequence selected from the group consisting of:

a nucleic acid sequence of any of SEQ ID Nos. 1-15; a nucleic acid sequence complementary to any of SEQ ID Nos. 1-15; a nucleic acid sequence having a degree of identity of more than 70% to any of SEQ ID Nos. 1-15 or to a sequence complementary to any of SEQ ID Nos. 1-15; alleles of the nucleic acid sequence of any of SEQ ID Nos. 1-15; alleles of a sequence complementary to any of SEQ ID Nos. 1-15; alleles of a nucleic acid sequence having a degree of identity of more than 70% to any of SEQ ID Nos. 1-15; and alleles of a nucleic acid sequence having a degree of identity of more than 70% to a sequence complementary to any of SEQ ID Nos. 1-15.

~~61.~~(New) A composition of matter comprising seeds, propagation material, harvest material, or plant tissue, wherein the composition includes a host cell containing a vector comprising a nucleic acid sequence selected from the group consisting of:

a nucleic acid sequence of any of SEQ ID Nos. 1-15; a nucleic acid sequence complementary to any of SEQ ID Nos. 1-15; a nucleic acid sequence having a degree of identity of more than 70% to any of SEQ ID Nos. 1-15 or to a sequence complementary to any of SEQ ID Nos. 1-15; alleles of the nucleic acid sequence of any of SEQ ID Nos. 1-15; alleles of a sequence complementary to any of SEQ ID Nos. 1-15; alleles of a nucleic acid sequence having a degree of identity of more than 70% to any of SEQ ID Nos. 1-15; and alleles of a nucleic acid sequence having a

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degree of identity of more than 70% to a sequence complementary to any of SEQ ID Nos. 1-15.

*A<sup>2</sup> cont'd*

~~62.~~ (New) A composition of matter comprising seeds, propagation material, harvest material, or plant tissue derived from a plant having a host cell containing a vector comprising a nucleic acid sequence selected from the group consisting of: a nucleic acid sequence of any of SEQ ID Nos. 1-15; a nucleic acid sequence complementary to any of SEQ ID Nos. 1-15; a nucleic acid sequence having a degree of identity of more than 70% to any of SEQ ID Nos. 1-15 or to a sequence complementary to any of SEQ ID Nos. 1-15; alleles of the nucleic acid sequence of any of SEQ ID Nos. 1-15; alleles of a sequence complementary to any of SEQ ID Nos. 1-15; alleles of a nucleic acid sequence having a degree of identity of more than 70% to any of SEQ ID Nos. 1-15; and alleles of a nucleic acid sequence having a degree of identity of more than 70% to a sequence complementary to any of SEQ ID Nos. 1-15.

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~~63.~~ (New) A method of genetically modifying a cell, comprising a step of transforming the cell with a nucleic acid sequence selected from the group consisting of: a nucleic acid sequence of any of SEQ ID Nos. 1-15; a nucleic acid sequence complementary to any of SEQ ID Nos. 1-15; a nucleic acid sequence having a degree of identity of more than 70% to any of SEQ ID Nos. 1-15 or to a sequence complementary to any of SEQ ID Nos. 1-15; alleles of the nucleic acid sequence of any of SEQ ID Nos. 1-15; alleles of a sequence complementary to any of SEQ ID Nos. 1-15; alleles of a nucleic acid sequence having a degree of identity of more than 70% to any of SEQ ID Nos. 1-15; and alleles of a nucleic acid sequence having a degree of identity of more than 70% to a sequence complementary to any of SEQ ID Nos. 1-15; wherein a gene of interest contained in the vector is expressible in the cell.

64.(New) The method of Claim 63, wherein the cell is a plant, bacterial, or yeast cell.

*sub 59* 65. (New) The method of Claim 63, containing a further step of regenerating the transformed cell to produce a differentiated plant.

*62 control* 66.(New) The method of Claim 63, wherein the step of transforming is accomplished by transfer of a vector or of nucleic acid sequences from a bacterium to the cell.

*sub 61* 67. (New) The method of Claim 63, wherein the step of transforming of the cell further includes either a step of microinjection with a vector or nucleic acid sequence or a step of particle bombardment with a vector or nucleic acid sequence, such that the step of transforming is accomplished by direct intake of a vector or nucleic acid sequence.

*68* 68. (New) A method for isolating a root specific gene and/or a root specific regulatory element from a plant, in which nucleic acid sequences derived from the plant are screened using a nucleic acid sequence selected from the group consisting of : a nucleic acid sequence of any of SEQ ID Nos. 1-15; a nucleic acid sequence complementary to any of SEQ ID Nos. 1-15; a nucleic acid sequence having a degree of identity of more than 70% to any of SEQ ID Nos. 1-15 or to a sequence complementary to any of SEQ ID Nos. 1-15; alleles of the nucleic acid sequence of any of SEQ ID Nos. 1-15; alleles of a sequence complementary to any of SEQ ID Nos. 1-15; alleles of a nucleic acid sequence having a degree of identity of more than 70% to any of SEQ ID Nos. 1-15; alleles of a nucleic acid sequence having a degree of identity of more than 70% to a sequence complementary to any of SEQ ID Nos. 1-15; and a vector comprising any of the preceding nucleic acid sequences and alleles.

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